PCT09

RAW SEQUENCE LISTING   DATE: 01/22/2002
PATENT APPLICATION: US/09/890,729   TIME: 10:17:23

Input Set : A:\A-579B.ST25.txt
Output Set: N:\CRF3\01182002\I890729.raw

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 3 <110> APPLICANT: Yoshinaga, Steven
 4        Mak, Tak
 5        Shahinian, Arda
 6        Trafuri Bladt, Anna
 7        Senaldi, Giorgio
 9 <120> TITLE OF INVENTION: Polypeptides Involved in Immune Response
11 <130> FILE REFERENCE: A-579B
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/890,729
C--> 13 <141> CURRENT FILING DATE: 2000-01-27
13 <150> PRIOR APPLICATION NUMBER: 09/890,729
14 <151> PRIOR FILING DATE: 2000-01-27
16 <150> PRIOR APPLICATION NUMBER: PCT/US00/01871
17 <151> PRIOR FILING DATE: 2000-01-27
19 <150> PRIOR APPLICATION NUMBER: US 09/264,527
20 <151> PRIOR FILING DATE: 1999-03-08
22 <150> PRIOR APPLICATION NUMBER: US 09/244,448
23 <151> PRIOR FILING DATE: 1999-02-03
25 <160> NUMBER OF SEQ ID NOS: 35
27 <170> SOFTWARE: PatentIn version 3.0
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31 <212> TYPE: DNA
32 <213> ORGANISM: Mus musculus
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44 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
45             20                  25                  30
47 ttt cac aat gga ggt gta cag att tct tgt aaa tac cct gag act gtc       144
48 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
49         35                  40                  45
51 cag cag tta aaa atg cga ttg ttc aga gag aga gaa gtc ctc tgc gaa       192
52 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
53     50                  55                  60
55 ctc acc aag acc aag gga agc gga aat gcg gtg tcc atc aag aat cca       240
56 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
57 65                  70                  75                  80
59 atg ctc tgt cta tat cat ctg tca aac aac agc gtc tct ttt ttc cta       288
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60 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
61                 85                  90                  95
63 aac aac cca gac agc tcc cag gga agc tat tac ttc tgc agc ctg tcc     336
64 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
65             100                 105                 110
67 att ttt gac cca cct cct ttt caa gaa agg aac ctt agt gga gga tat     384
68 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
69         115                 120                 125
71 ttg cat att tat gaa tcc cag ctc tgc tgc cag ctg aag ctc tgg cta     432
72 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
73     130                 135                 140
75 ccc gta ggg tgt gca gct ttc gtt gtg gta ctc ctt ttt gga tgc ata     480
76 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
77 145                 150                 155                 160
79 ctt atc atc tgg ttt tca aaa aag aaa tac gga tcc agt gtg cat gac     528
80 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
81                 165                 170                 175
83 cct aat agt gaa tac atg ttc atg gcg gca gtc aac aca aac aaa aag     576
84 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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87 tct aga ctt gca ggt gtg acc tca                                     600
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93 <211> LENGTH: 200
94 <212> TYPE: PRT
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103 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
104             20                  25                  30
107 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
108         35                  40                  45
111 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
112     50                  55                  60
115 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
116 65                  70                  75                  80
119 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
120                 85                  90                  95
123 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
124             100                 105                 110
127 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
128         115                 120                 125
131 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
132     130                 135                 140
135 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
136 145                 150                 155                 160
139 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
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156 <400> SEQUENCE: 3
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161 Leu Leu Thr Gly Glu Ile Asn Gly Ser Ala Asp His Arg Met Phe Ser
162             20                 25                  30
164 Phe His Asn Gly Gly Val Gln Ile Ser Cys Lys Tyr Pro Glu Thr Val
165          35                 40                  45
167 Gln Gln Leu Lys Met Arg Leu Phe Arg Glu Arg Glu Val Leu Cys Glu
168       50                 55                  60
170 Leu Thr Lys Thr Lys Gly Ser Gly Asn Ala Val Ser Ile Lys Asn Pro
171 65                 70                 75                  80
173 Met Leu Cys Leu Tyr His Leu Ser Asn Asn Ser Val Ser Phe Phe Leu
174             85                 90                  95
176 Asn Asn Pro Asp Ser Ser Gln Gly Ser Tyr Tyr Phe Cys Ser Leu Ser
177          100                105                 110
179 Ile Phe Asp Pro Pro Pro Phe Gln Glu Arg Asn Leu Ser Gly Gly Tyr
180          115                120                 125
182 Leu His Ile Tyr Glu Ser Gln Leu Cys Cys Gln Leu Lys Leu Trp Leu
183       130                135                 140
185 Pro Val Gly Cys Ala Ala Phe Val Val Val Leu Leu Phe Gly Cys Ile
186 145                150                 155                 160
188 Leu Ile Ile Trp Phe Ser Lys Lys Lys Tyr Gly Ser Ser Val His Asp
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191 Pro Asn Ser Glu Tyr Met Phe Met Ala Ala Val Asn Thr Asn Lys Lys
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208             20                 25                  30
210 Asp Ser Asn Glu Val Ser Leu Ser Cys Arg Tyr Ser Tyr Asn Leu Leu
211          35                 40                  45
213 Ala Lys Glu Phe Arg Ala Ser Leu Tyr Lys Gly Val Asn Ser Asp Val
214       50                 55                  60
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216 Glu Val Cys Val Gly Asn Gly Asn Phe Thr Tyr Gln Pro Gln Phe Arg
217 65                  70              75                  80
219 Ser Asn Ala Glu Phe Asn Cys Asp Gly Asp Phe Asp Asn Glu Thr Val
220              85              90                  95
222 Thr Phe Arg Leu Trp Asn Leu His Val Asn His Thr Asp Ile Tyr Phe
223             100             105             110
225 Cys Lys Ile Glu Phe Met Tyr Pro Pro Tyr Leu Asp Asn Glu Arg
226         115             120             125
228 Ser Asn Gly Thr Ile Ile His Ile Lys Glu Lys His Leu Cys His Thr
229     130             135             140
231 Gln Ser Ser Pro Lys Leu Phe Trp Ala Leu Val Val Val Ala Gly Val
232 145             150             155             160
234 Leu Phe Cys Tyr Gly Leu Leu Val Thr Val Ala Leu Cys Val Ile Trp
235             165             170             175
237 Thr Asn Ser Arg Arg Asn Arg Leu Leu Gln Val Thr Thr Met Asn Met
238             180             185             190
240 Thr Pro Arg Arg Pro Gly Leu Thr Arg Lys Pro Tyr Gln Pro Tyr Ala
241         195             200             205
243 Pro Ala Arg Asp Phe Ala Ala Tyr Arg Pro
244     210             215
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247 <211> LENGTH: 44
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial sequence
251 <220> FEATURE:
252 <221> NAME/KEY: misc_feature
253 <223> OTHER INFORMATION: Synthetic
256 <400> SEQUENCE: 5
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261 Asn Tyr Phe Cys Pro Pro Pro Ser Gly His Ile Glu Leu Cys Lys Leu
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264 Trp Leu Val Phe Leu Leu Leu Ile Trp Pro Arg Ala
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269 <212> TYPE: DNA
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273 <221> NAME/KEY: CDS
274 <222> LOCATION: (1)..(966)
276 <400> SEQUENCE: 6
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279 1           5               10              15
281 gtt tgg aag aag ctc cat gtt tct agc ggg ttc ttt tct ggt ctt ggt      96
282 Val Trp Lys Lys Leu His Val Ser Ser Gly Phe Phe Ser Gly Leu Gly
283             20              25              30
285 ctg ttc ttg ctg ctg ttg agc agc ctc tgt gct gcc tct gca gag act     144
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Input Set : A:\A-579B.ST25.txt
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286 Leu Phe Leu Leu Leu Leu Ser Ser Leu Cys Ala Ala Ser Ala Glu Thr
287         35                  40                  45
289 gaa gtc ggt gca atg gtg ggc agc aat gtg gtg ctc agc tgc att gac      192
290 Glu Val Gly Ala Met Val Gly Ser Asn Val Val Leu Ser Cys Ile Asp
291     50                  55                  60
293 ccc cac aga cgc cat ttc aac ttg agt ggt ctg tat gtc tat tgg caa      240
294 Pro His Arg Arg His Phe Asn Leu Ser Gly Leu Tyr Val Tyr Trp Gln
295 65                  70                  75                  80
297 atc gaa aac cca gaa gtt tcg gtg act tac tac ctg cct tac aag tct      288
298 Ile Glu Asn Pro Glu Val Ser Val Thr Tyr Tyr Leu Pro Tyr Lys Ser
299                 85                  90                  95
301 cca ggg atc aat gtg gac agt tcc tac aag aac agg ggc cat ctg tcc      336
302 Pro Gly Ile Asn Val Asp Ser Ser Tyr Lys Asn Arg Gly His Leu Ser
303                 100                 105                 110
305 ctg gac tcc atg aag cag ggt aac ttc tct ctg tac ctg aag aat gtc      384
306 Leu Asp Ser Met Lys Gln Gly Asn Phe Ser Leu Tyr Leu Lys Asn Val
307         115                 120                 125
309 acc cct cag gat acc cag gag ttc aca tgc cgg gta ttt atg aat aca      432
310 Thr Pro Gln Asp Thr Gln Glu Phe Thr Cys Arg Val Phe Met Asn Thr
311     130                 135                 140
313 gcc aca gag tta gtc aag atc ttg gaa gag gtg gtc agg ctg cgt gtg      480
314 Ala Thr Glu Leu Val Lys Ile Leu Glu Glu Val Val Arg Leu Arg Val
315 145                 150                 155                 160
317 gca gca aac ttc agt aca cct gtc atc agc acc tct gat agc tcc aac      528
318 Ala Ala Asn Phe Ser Thr Pro Val Ile Ser Thr Ser Asp Ser Ser Asn
319                 165                 170                 175
321 ccg ggc cag gaa cgt acc tac acc tgc atg tcc aag aat ggc tac cca      576
322 Pro Gly Gln Glu Arg Thr Tyr Thr Cys Met Ser Lys Asn Gly Tyr Pro
323                 180                 185                 190
325 gag ccc aac ctg tat tgg atc aac aca acg gac aat agc cta ata gac      624
326 Glu Pro Asn Leu Tyr Trp Ile Asn Thr Thr Asp Asn Ser Leu Ile Asp
327                 195                 200                 205
329 acg gct ctg cag aat aac act gtc tac ttg aac aag ttg ggc ctg tat      672
330 Thr Ala Leu Gln Asn Asn Thr Val Tyr Leu Asn Lys Leu Gly Leu Tyr
331     210                 215                 220
333 gat gta atc agc aca tta agg ctc cct tgg aca tct cgt ggg gat gtt      720
334 Asp Val Ile Ser Thr Leu Arg Leu Pro Trp Thr Ser Arg Gly Asp Val
335 225                 230                 235                 240
337 ctg tgc tgc gta gag aat gtg gct ctc cac cag aac atc act agc att      768
338 Leu Cys Cys Val Glu Asn Val Ala Leu His Gln Asn Ile Thr Ser Ile
339                 245                 250                 255
341 agc cag gca gaa agt ttc act gga aat aac aca aag aac cca cag gaa      816
342 Ser Gln Ala Glu Ser Phe Thr Gly Asn Asn Thr Lys Asn Pro Gln Glu
343                 260                 265                 270
345 acc cac aat aat gag tta aaa gtc ctt gtc ccc gtc ctt gct gta ctg      864
346 Thr His Asn Asn Glu Leu Lys Val Leu Val Pro Val Leu Ala Val Leu
347         275                 280                 285
349 gcg gca gcg gca ttc gtt tcc ttc atc ata tac aga cgc acg cgt ccc      912
350 Ala Ala Ala Ala Phe Val Ser Phe Ile Ile Tyr Arg Arg Thr Arg Pro
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/890,729

DATE: 01/22/2002
TIME: 10:17:24

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L:1303 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21